

M. RAO

#26



1600

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RAW SEQUENCE LISTING

DATE: 11/08/2002

PATENT APPLICATION: US/09/339,159B

TIME: 10:52:52

Input Set : A:\sequence2.ST25.txt

Output Set: N:\CRF4\11082002\I339159B.raw

3 <110> APPLICANT: Kauppinen, Markus
 4 Schulein, Martin
 5 Schnorr, Kirk
 6 Andersen, Lene
 7 Bjornvad, Mads
 9 <120> TITLE OF INVENTION: Novel Mannanases
 11 <130> FILE REFERENCE: 5440.204-US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/339,159B
 C--> 13 <141> CURRENT FILING DATE: 1999-06-24
 13 <160> NUMBER OF SEQ ID NOS: 55
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1470
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Bacillus sp. I633
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 25 attctgttcg tttcaggaac ttctacagct aatgcaaatt ccggatttta tgtaagcgg 120
 27 accactctat acgatgccaa tggaaaccca tttgtaatga gagggattaa ccatgggcac 180
 29 gcatggtata aagaccaggc aactactgca attgaaggga ttgcaaatac cgggtgcta 240
 31 acggtccgga ttgtgttatc tgatggggga caatggacaa aagatgacat ccatacagta 300
 33 agaaacctta tctcttttagc ggaagataat catttggttg ctgttcttga agttcatgat 360
 35 gctaccgggt atgattccat tgcttcgctc aatcgtgctg ttgattattg gattgaaatg 420
 37 agaagtgcct taattggaaa ggaagatacc gtcattatta atattgcgaa tgaatgggtt 480
 39 gggttcgtggg aaggggtagc ttgggctgac ggtataaac aagcaatccc gcgattgcgt 540
 41 aacgccgggtc taaaccatac cttgatggta gatgctgcgg ggtggggaca atttccacaa 600
 43 tcgattcatg attatggaag agaagttttt aatgctgacc ctcaacgaaa tacaatgttt 660
 45 tcgattcata tgtatgaata tgcagggtgt aatgcatcgc aagttcgtac taatattgac 720
 47 cgagttctta atcaagacct cgcattagtc attggtgaat ttggacaccg tcatacaaat 780
 49 ggtgacgtcg atgaagcaac gattatgagc tattctgaac aaagaggagt tgggtggttg 840
 51 gcgtgggtcat ggaaagggaa cggcccagaa tgggagtatt tagacctttc gaatgattgg 900
 53 gctggaaata accttacagc ttggggaaat acaatagtga atggtccata tggtttaaga 960
 55 gaaacttcga gattaagcac cgtttttaca ggtggaggat ctgatggagg aacttctccg 1020
 57 acaactcttt atgattttga aggtagtatg caaggatgga ctggaagtag cttgagcgga 1080
 59 ggtccttggg ctgtgacaga gtggtcttct aaaggaaatc attctttaaa agcggatatt 1140
 61 caattgtcgt caaattcaca acattactta catgttattc aaaatacgtc tttacagcag 1200
 63 aatagtagga tacaagctac tgtaaacaat gcaaattggg gaagtgttg taatggaatg 1260
 65 actgcgcgtc tttatgtgaa aacaggacat ggttatacat ggtactctgg aagctttgtg 1320
 67 ccgattaacg gttcatctgg aacaacgcta tctctagatt tatcaaatgt ccaaaatctt 1380
 69 tctcaagtaa gggaaattgg agttcagttc caatcagcga gtgatagtag tggacaaaca 1440
 71 tcgatttata ttgataatgt gattgtagaa 1470
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 490

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76 <212> TYPE: PRT

77 <213> ORGANISM: Bacillus

79 <400> SEQUENCE: 2

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81 Leu Asn Asn Gly Phe Lys Lys Ile Phe Ser Ile Thr Leu Ser Leu Leu
82 1          5          10          15
85 Leu Ala Ser Ser Ile Leu Phe Val Ser Gly Thr Ser Thr Ala Asn Ala
86          20          25          30
89 Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly
90          35          40          45
93 Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
94          50          55          60
97 Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn
98 65          70          75          80
101 Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp
102          85          90          95
105 Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu
106          100          105          110
109 Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala
110          115          120          125
113 Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu
114          130          135          140
117 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe
118 145          150          155          160
121 Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile
122          165          170          175
125 Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala
126          180          185          190
129 Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu
130          195          200          205
133 Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met
134          210          215          220
137 Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp
138 225          230          235          240
141 Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
142          245          250          255
145 Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser
146          260          265          270
149 Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly
150          275          280          285
153 Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn Asn
154          290          295          300
157 Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu Arg
158 305          310          315          320
161 Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly
162          325          330          335
165 Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly
166          340          345          350
169 Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp
170          355          360          365

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Input Set : A:\sequence2.ST25.txt

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173 Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser
 174 370 375 380
 177 Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln
 178 385 390 395 400
 181 Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val
 182 405 410 415
 185 Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr
 186 420 425 430
 189 Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr
 190 435 440 445
 193 Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg
 194 450 455 460
 197 Glu Ile Gly Val Gln Phe Gln Ser Ala Ser Asp Ser Ser Gly Gln Thr
 198 465 470 475 480
 201 Ser Ile Tyr Ile Asp Asn Val Ile Val Glu
 202 485 490

205 <210> SEQ ID NO: 3

206 <211> LENGTH: 1438

207 <212> TYPE: DNA

208 <213> ORGANISM: Bacillus sp. I633

210 <400> SEQUENCE: 3

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 213 gtaatgagag ggattaacca tgggcacgca tgggtataaag accaggcaac tactgcaatt 120
 215 gaaggggattg caaataaccgg tgctaataacg gtccggattg tggtatctga tgggggacaa 180
 217 tggacaaaag atgacatcca tacagtaaga aaccttatct ctttagcggg agataatcat 240
 219 ttggttgctg ttctgaagt tcatgatgct accggttatg attccattgc ttcgctcaat 300
 221 cgtgctggtg attattggat tgaaatgaga agtgctttta ttggaaagga agataccgctc 360
 223 attattaata ttgcgaatga atggtttggg tcgtgggaag gggatgcttg ggctgacggg 420
 225 tataaacaag caatcccgcg attgcgtaac gccggtctaa accatacctt gatggtagat 480
 227 gctgcgggggt ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540
 229 gctgaccctc aacgaaatac aatgttttcg attcatatgt atgaatatgc aggtggtaat 600
 231 gcatcgcaag ttctgactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660
 233 ggtgaatttg gacaccgtca tacaatggg gacgtcgatg aagcaacgat tatgagctat 720
 235 tctgaacaaa gaggagttgg gtggttggcg tggatcatgga aagggaacgg cccagaatgg 780
 237 gagtatttag acctttcgaa tgattgggct ggaaataacc ttacagcttg gggaaataca 840
 239 atagtgaatg gtccatatgg tttaagagaa acttcgagat taagcaccgt ttttacagct 900
 241 agcccggaac caacaccaga gccgaccgca aatacaccgg tatcaggcaa tttgaagggt 960
 243 gaattctaca acagcaatcc ttcagatact actaactcaa tcaatcctca gttcaagggt 1020
 245 actaataaccg gaagcagtg c aattgatttg tccaaactca cattgagata ttattataca 1080
 247 gtagacggac agaaagatca gaccttctgg tgtgaccatg ctgcaataat cggcagtaac 1140
 249 ggcagctaca acggaattac ttcaaattga aaaggaacat ttgtaaaaat gagttcctca 1200
 251 acaaataacg cagacaccta ccttgaaata agctttacag gcggaactct tgaaccgggt 1260
 253 gcacatgttc agatacaagg tagatttgca aagaatgact ggagtaacta tacacagtca 1320
 255 aatgactact cattcaagtc tcgttcacag tttgttgaat gggatcaggt aacagcatac 1380
 257 ttgaacgggt ttcttgtatg gggtaaagaa cccggtggca gtgtagtata gcggccgc 1438

260 <210> SEQ ID NO: 4

261 <211> LENGTH: 476

262 <212> TYPE: PRT

263 <213> ORGANISM: Bacillus

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268 1 5 10 15
271 Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr
272 20 25 30
275 Lys Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala
276 35 40 45
279 Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp
280 50 55 60
283 Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His
284 65 70 75 80
287 Leu Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile
288 85 90 95
291 Ala Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala
292 100 105 110
295 Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp
296 115 120 125
299 Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala
300 130 135 140
303 Ile Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp
304 145 150 155 160
307 Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg
308 165 170 175
311 Glu Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His
312 180 185 190
315 Met Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile
316 195 200 205
319 Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly
320 210 215 220
323 His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr
324 225 230 235 240
327 Ser Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn
328 245 250 255
331 Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn
332 260 265 270
335 Asn Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu
336 275 280 285
339 Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro
340 290 295 300
343 Thr Pro Glu Pro Thr Ala Asn Thr Pro Val Ser Gly Asn Leu Lys Val
344 305 310 315 320
347 Glu Phe Tyr Asn Ser Asn Pro Ser Asp Thr Thr Asn Ser Ile Asn Pro
348 325 330 335
351 Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys
352 340 345 350
355 Leu Thr Leu Arg Tyr Tyr Tyr Thr Val Asp Gly Gln Lys Asp Gln Thr
356 355 360 365
359 Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn
360 370 375 380

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363 Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser
364 385                               390                               395                               400
367 Thr Asn Asn Ala Asp Thr Tyr Leu Glu Ile Ser Phe Thr Gly Gly Thr
368                               405                               410                               415
371 Leu Glu Pro Gly Ala His Val Gln Ile Gln Gly Arg Phe Ala Lys Asn
372                               420                               425                               430
375 Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg
376                               435                               440                               445
379 Ser Gln Phe Val Glu Trp Asp Gln Val Thr Ala Tyr Leu Asn Gly Val
380                               450                               455                               460
383 Leu Val Trp Gly Lys Glu Pro Gly Gly Ser Val Val
384 465                               470                               475
387 <210> SEQ ID NO: 5
388 <211> LENGTH: 1482
389 <212> TYPE: DNA
390 <213> ORGANISM: Bacillus agaradhaerens
392 <400> SEQUENCE: 5
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395 ggaataatgg ggattacaac gtcccatca gcagcaagta caggctttta tgttgatggc      120
397 aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat      180
399 gcttgggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac      240
401 acgattcgtta ttgttttatc agatggcggg caatgggaaa aagacgacat tgacaccatt      300
403 cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat      360
405 gccacgggtc gcgattcgcg cagtgtattt aatcgagccg ttgattattg gatagaaatg      420
407 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat      480
409 gggagttggg atggctcagc ttgggccgat ggctatattg atgtcattcc gaagcttcgc      540
411 gatgccggct taacacacac cttaatggtt gatgcagcag gatgggggca atatccgcaa      600
413 tctattcatg attacggaca agatgtgttt aatgcagatc cgtaaaaaaa tacgatgttc      660
415 tccatccata tgtatgagta tgctgtgtgt gatgctaaca ctgttagatc aaatattgat      720
417 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat      780
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421 gcttgggtctt ggaaaggcaa cagtaccgaa tgggactatt tagacccttc agaagactgg      900
423 gctgggtcaac atttaactga ttgggggaat agaattgtcc acggggccga tggcttacag      960
425 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcaccc tgaaccgcca      1020
427 actgctacta ctttgtatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg      1080
429 accggtggcc cttggtccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc      1140
431 gatgtaaatt taacctcaaa ttcttcacat gaactgtata gtgaacaaag tcgtaaatcta      1200
433 cacggatact ctcagctcaa cgcaaccggt cgccatgcca attggggaaa tcccggtaat      1260
435 ggcatgaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcggtcct      1320
437 ttacacgta tcaatagctc caactcagga acaacgttat cttttgattt aaacaacatc      1380
439 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt      1440
441 ggtcaaactg ctctatacgt tgataacggt actttaagat ag                               1482
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445 <211> LENGTH: 493
446 <212> TYPE: PRT
447 <213> ORGANISM: Bacillus
449 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

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Input Set : A:\sequence2.ST25.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date